

Atty Dkt. No.: TGEN-001
USSN: 09/471,703

70. (New) The method of claim 69, wherein the primer hybridizes to the target sequence such that its 3' end is immediately upstream of the variant nucleotide.

71. (New) The method of claim 69, wherein the primer hybridizes to the target sequence such that its 3' end is 2 or more nucleotides 5' of the variant nucleotide.

72. (New) The method of claim 69, wherein said analyzing comprises determining the length of said reaction products.

73. (New) The method of claim 69, wherein said analyzing comprises performing a technique selected from the group consisting of chromatography, capillary electrophoresis, microfluidic analysis, and slab gel electrophoresis.

74. (New) The method of claim 69, wherein said analyzing comprises performing high performance liquid chromatography.

75. (New) The method of claim 69, wherein said analyzing comprises performing capillary electrophoresis.

76. (New) The method of claim 69, wherein said analyzing reaction products comprises determining the identity of a nucleotide incorporated in a reaction product.

77. (New) The method of claim 69, wherein said analyzing comprises use of an intercalating agent.

78. (New) The method of claim 77, wherein the intercalating agent is ethidium bromide.

79. (New) The method of claim 77, wherein the intercalating agent is an unsymmetrical cyanine dye.

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80. (New) The method of claim 69, wherein said analyzing comprises use of slab electrophoresis and ultraviolet light.

81. (New) The method of claim 69, wherein the reaction products are detected using slab electrophoresis and a DNA-binding dye.

82. (New) The method of claim 69, wherein the target sequence comprises a biallelic marker associated with genetic disorders.

83. (New) The method of claim 69, wherein the target sequence is present in a sample obtained from a diploid organism.

84. (New) A method for screening a DNA sample for a plurality of target sequences having at least two known variants, comprising:

contacting a sample comprising a plurality of known target sequences with an extension reaction mixture, the mixture comprising

a primer that specifically hybridizes to a target sequence of interest such that the 3' end of the primer is at least one nucleotide 5' of a variant nucleotide of the polymorphic site, and

a plurality of deoxyribonucleoside triphosphates (dNTP) or ribonucleoside triphosphates (rNTP), where the plurality of dNTPs or rNTPs provide for at least one nucleotide extension of the primer when hybridized to a target sequence having either of the two variant nucleotides,

the mixture excluding a dideoxynucleoside triphosphate (ddNTP) and further excluding a dNTP or rNTP complementary to one of said variant nucleotides of the SNP, wherein the dNTPs or rNTPs in the mixture are not detectably labeled or modified; and

analyzing the reaction products of each extension reaction.

85. (New) The method of claim 84, wherein the target sequence is associated with genetic disorders.

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86. (New) The method of claim 84, wherein the sample is from a diploid organism.

87. (New) The method of claims 84, wherein the extension reaction mixture comprises a plurality of different primers, which primers specifically hybridize to different target sequences, wherein each primer is of a length or sequence such that extension products of the different primers can be distinguished one from another.

88. (New) The method of claim 87, wherein the different primers are of different lengths.